us-09-987-701-2.rsp

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181 SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL 240
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-> H (IN REF. 3).
-> Q (IN REF. 2).
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1; Mismatches
                                          PROSITE; PS50896; LISH; 1.
PROSITE; PS06049; WD REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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WD 1.

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59
389
                                  SMART; SM00320; WD40;
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REPEAT 223 22

REPEAT 264 33

REPEAT 346 34

REPEAT 347 440 44

REPEAT 441 55
                                                                                                                                                                                                                                                                     514 AA;
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16-0CT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
LOCT-2003 (Rel. 42, Last annotation update)
Transducin beta-like 1X protein (Transducin-beta-like 1, X-linked)

PRT; 526 AA.

STANDARD;

HUMAN

TBLX

060907;

mo sapiens (Human). Maryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

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                                                                                       MEDLINE=99264241; PubMed=10330347;
Bassi M.T., Ramesar R.S., Caciotti B., Winship I.M., De Grandi A.,
Riboni M., Townes P.L., Beighton P., Ballabio A., Borsani G.;
"X-linked late-onest sensorineural deafness caused by a deletion involving OA1 and a novel gene containing WD-40 repeats.";
Am. J. Hum. Genet. 64:1604-1616(1999).
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSS0896; LISH; 1.
PROSITE; PSS00678; WD_REPEATS_1; 4.
PROSITE; PSS0082; WD_REPEATS_2; 6.
PROSITE; PSS0294; WD_REPEATS_REGION; 1.
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Genew; HGNC:11585; TBL1X.
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      NCBI_TaxID=9606;
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Kuroda-Kawaguchi T., Skaletsky H., Minx P.J., Brown L.G., Rozen S.,
Wilson R.K., Waterston R.H., Page D.C.,
"The DNA sequence of the human Y chromosome.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 LisH domain.
-!- SIMILARITY: Contains 8 WD repeats.
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28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Transducin beta-like 1Y protein (Transducin-beta-like 1, Y-linked)
TBLIY OR TBLIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                         14;
                                                                                               89.4%; Score 2437; DB 1; Length 526; 86.0%; Pred. No. 2.1e-168; Live 33; Mismatches 27; Indels 1
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Mammalia, Eutheria, Primates,
                                                                                                                                                 453; Conservative
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526 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 -----AAASQQGSAKNGENTANGEENGAHTIANNHIDNMEVDGDVEIPPNKAVVLRGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AATWTPAAISQONPPKAREATVNGEENGAHEI-NNHSKPWEIDGDVBIPPNKATVLRGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 SEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 SEVFICAWNPVSDLLASGSGDSTARIWNINENSNGGSTQLVLRHCIREGGHDVPSNKDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 SLDWNSEGTLLATGSYDGFARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIIWDAHTGEAKQOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 BAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDL 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4E020216422442D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.8%; Score 2367; DB 1;
llarity 84.5%; Pred. No. 2.4e-163;
Conservative 35; Mismatches 34;
                                EMBL, AF332220; AAK134721; ---
EMBL, AF332220; AAK134731; ---
EMBL, AF332222 AAK134731; ---
Genew, HGNC.18502; ARI34741; ---
InterPro; IPR006594; LisH.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; WD40.
ProDom; PD000018; WD40; B.
PRODOM; PD000018; WD40; 3.
SMART; SM00667; LisH; 1.
SMART; SM00678; WD40; 8.
PROSITE; PS50996; LISH; 1.
PROSITE; PS50096; WD REPEATS 1; 4.
PROSITE; PS50094; WD REPEATS 2; 6.
PROSITE; PS50094; WD REPEATS 2; 6.
PROSITE; PS50094; WD REPEATS 2; 6.
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                       LISH.
WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3354
4447
489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491 5
522 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 442; Conserv
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Ä 313